



1600

RAW SEQUENCE LISTING

DATE: 02/10/2003

PATENT APPLICATION: US/09/688,286C

TIME: 14:53:01

Input Set : A:\11373a.txt

Output Set: N:\CRF4\02102003\I688286C.raw

3 <110> APPLICANT: Willson, Tracy
4 Nicola, Nicos A.
5 Hilton, Douglas J.
6 Metcalf, Donald
7 Zhang, Jian G.
9 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
10 ENCODING SAME
12 <130> FILE REFERENCE: 11373a
14 <140> CURRENT APPLICATION NUMBER: 09/688,286C
15 <141> CURRENT FILING DATE: 2000-10-31
17 <160> NUMBER OF SEQ ID NOS: 12
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1383
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (61)..(1338)
30 <220> FEATURE:
31 <221> NAME/KEY: unsure
32 <222> LOCATION: (121)
33 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
34 region
36 <220> FEATURE:
37 <221> NAME/KEY: unsure
38 <222> LOCATION: (122)
39 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
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44 <222> LOCATION: (123)
45 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
46 region
48 <220> FEATURE:
49 <221> NAME/KEY: unsure
50 <222> LOCATION: (640)
51 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
52 region
55 <220> FEATURE:
56 <221> NAME/KEY: unsure
57 <222> LOCATION: (641)
58 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this

ENTERED

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62 <221> NAME/KEY: unsure
63 <222> LOCATION: (642)
64 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
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70 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
71 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Trp
72 1 5 10 15
W--> 74 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
75 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Thr Glu Val Gln Pro
76 20 25 30
78 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
79 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
80 35 40 45
82 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
83 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
84 50 55 60
86 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
87 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
88 65 70 75 80
90 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
91 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
92 85 90 95
94 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
95 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
96 100 105 110
98 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
99 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
100 115 120 125
102 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
103 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
104 130 135 140
106 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
107 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
108 145 150 155 160
110 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
111 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
112 165 170 175
114 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
115 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
116 180 185 190
118 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684
119 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
120 195 200 205
122 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
123 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr

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124      210      215      220
126 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt 780
127 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
128 225      230      235      240
130 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc 828
131 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
132      245      250      255
134 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat 876
135 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
136      260      265      270
138 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga 924
139 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
140      275      280      285
142 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac 972
143 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
144      290      295      300
146 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt 1020
147 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
148 305      310      315      320
150 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt 1068
151 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
152      325      330      335
154 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca 1116
155 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
156      340      345      350
158 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg 1164
159 Val Phe Val Ala Val Ala Val Ile Leu Leu Phe Tyr Leu Lys Arg
160      355      360      365
162 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt 1212
163 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
164      370      375      380
166 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag 1260
167 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
168 385      390      395      400
170 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg 1308
171 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
172      405      410      415
174 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc 1358
175 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
176      420      425
178 tttcttgacct tcaatgtgac cctgt 1383
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 426
183 <212> TYPE: PRT
184 <213> ORGANISM: Mus musculus
186 <220> FEATURE:
187 <221> NAME/KEY: unsure
188 <222> LOCATION: (21)
189 <223> OTHER INFORMATION: authors are unsure about the sequence assignment

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Input Set : A:\11373a.txt

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191 <220> FEATURE:

192 <221> NAME/KEY: unsure

193 <222> LOCATION: (194)

194 <223> OTHER INFORMATION: authors are unsure about the sequence assignment

196 <400> SEQUENCE: 2

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W--> 200 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
201           20           25           30
203 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
204           35           40           45
206 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
207           50           55           60
209 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
210           65           70           75           80
212 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
213           85           90           95
215 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
216           100          105          110
218 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
219           115          120          125
221 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
222           130          135          140
224 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
225           145          150          155          160
227 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
228           165          170          175
230 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
231           180          185          190
233 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
234           195          200          205
236 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
237           210          215          220
239 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
240           225          230          235          240
242 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
243           245          250          255
245 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
246           260          265          270
248 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
249           275          280          285
251 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
252           290          295          300
254 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
255           305          310          315          320
257 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
258           325          330          335
261 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
262           340          345          350

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264 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
265           355           360           365
267 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
268           370           375           380
270 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
271 385           390           395           400
273 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
274           405           410           415
276 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
277           420           425
280 <210> SEQ ID NO: 3
281 <211> LENGTH: 1383
282 <212> TYPE: DNA
283 <213> ORGANISM: Homo sapiens
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (61)..(1338)
290 <400> SEQUENCE: 3
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293 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
294 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
295 1 5 10 15
297 gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca 156
298 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
299 20 25 30
301 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
302 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
303 35 40 45
305 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
306 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
307 50 55 60
309 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
310 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
311 65 70 75 80
313 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
314 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
315 85 90 95
317 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
318 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
319 100 105 110
321 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
322 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
323 115 120 125
325 act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
326 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
327 130 135 140
329 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
330 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
331 145 150 155 160

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/688,286C

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Input Set : A:\11373a.txt
Output Set: N:\CRF4\02102003\I688286C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 121, 122, 123, 640, 641, 642
Seq#:1; Xaa Pos. 21, 194
Seq#:2; Xaa Pos. 21, 194
Seq#:9; Xaa Pos. 3
Seq#:10; Xaa Pos. 24
Seq#:11; Xaa Pos. 24